Claims

1. A method of determining the sequence and/or occurrence frequency of a number of variable gene inserts from a gene library which inserts exhibit a desired specific characteristic, wherein each variable gene insert is flanked 5' and 3' adjacent known sequences, the method comprising;

selecting the number of inserts by their ability to exhibit the desired specific characteristic, conducting polymerase chain reaction to amplify the selected number of variable gene inserts to produce components of a mixed PCR product;

ligating the components of the mixed PCR product to produce a concatenated sequence; and

sequencing or determining the occurrence of the gene inserts in the concatenated sequence.

2. A method as claimed in claim 1 wherein the gene library is a peptide phage display library.

3. A method as claimed in claim 1 or claim 2, wherein the components of the mixed PCR product are digested with a restriction endonuclease before ligation to produce the concatenated sequence.

4. A method as claimed in any one of claims 1 to 3, wherein the concatenated sequence is cloned into a plasmid before sequencing.

5. A method as claimed in claim 4, wherein the concatenated sequence is size selected to from around 500 to around 1.5 kilobases in length before cloning into the plasmid.

6. A method as claimed in any one of claims 2 to 5, wherein the length of each

variable gene inserts is from 18 to 36 nucleotides.

7. A method as claimed in claim 6, wherein the specific characteristic is one or more of protein binding or occurrence only in one state of tissue in a comparison with the same tissue in a different state.

8. A method as claimed in any one of claims 2 to 5, wherein the number of variable gene inserts are from phage which do not exhibit a specific characteristic.

9. A method as claimed in any one of claims 1 to 9, wherein selecting the number of inserts by their ability to exhibit the desired specific characteristic comprises two or more rounds of selection based on the ability of the variable gene inserts to exhibit the desired characteristic.

10. A method as claimed in any one of claims 1 to 9, wherein when more than one round of selection by the ability of the insert to exhibit the desired characteristic is carried out, then the different rounds of selection may be of more than one desired specific characteristic.

11. A method according to any one of the preceding claims, further comprising characterisation and/or quantitation of the target molecule.

12. A method according to claim 11, which uses fluorescence resonant energy transfer.

13. A data set of the sub-library resulting from the method of any one of the preceding claims.

14. A determination of the sequence or occurrence frequency of a number of variable gene inserts from a gene library, obtained by a method according to any one of claims 1 to 12.